SEQUENCE LISTING

- <110> The Curators of the University of Missouri
- <120> LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT PROTEINS
- <130> UMO1531.1
- <140>
- <141>
- <150> 60/218,125
- <151> 2000-01-13
- <160> 2
- <170> PatentIn Ver. 2.1
- <210> 1
- <211> 4087
- <212> DNA
- <213> Bos taurus
- <220>
- <221> CDS
- <222> (268)..(3180)
- <220>
- <221> sig_peptide
- <222> (268)..(363)
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- <221> misc feature
- <222> (3178)
- <223> A Poly (H) affinity tag comprising 6 His residues have been inserted at the C-Terminus end of the coding region of the protein
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- ggcgaacatc aactcgtgct tgaaaaatac caacttggag cccggtttga gaagctacat 180
- cagagteteg agatgegacg etacaatetg cagtttteac tagetteeca gtaggttggg 240

	, 5 ;	,		,				-	eu Gi	Ln Pl	ne Se	er Le	eu Se	er Pi	o Thr	
tta	tca	ato	gga	ttt	cac	ata	ata	acc	ato	ata	act	ctc	tta	ttt	tee	342
	_	_				-		_	_		_			Phe		7.2
10	Der	Mec	GLY	1110	15	Val	116	ALG	Mec	20	ALG	пец	Dea	1110	25	
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cat	gtg	gac	cat	ata	agt	gct	gag	aca	gaa	atg	gaa	gga	gaa	ggc	aac	390
His	Val	Asp	His	Ile	Ser	Ala	Glu	Thr	Glu	Met	Glu	Gly	Glu	Gly	Asn	
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gag	act	ggc	gag	tgt	act	ggc	tcc	tat	tac	tgt	aag	aag	ggg	gtg	att	438
Glu	Thr	Gly	Glu	Cys	Thr	Gly	Ser	Tyr	Tyr	Cys	Lys	Lys	Gly	Val	Ile	
		_	45	_		_		50	_	_	_	_	55			
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Leu	Pro	Ile	Trp	Glu	Pro	Gln	Asp	Pro	Ser	Phe	Gly	Asp	Lys	Ile	Ala	
		60					65					70				
aga	gcg	act	gtg	tat	ttt	gtg	gcc	atg	gtc	tac	atg	ttt	ctt	gga	gtc	534
Arg	Ala	Thr	Val	Tyr	Phe	Val	Ala	Met	Val	Tyr	Met	Phe	Leu	Gly	Val	
	75					80					85					
tca	atc	att	gct	gac	cgg	ttc	atg	tcc	tct	ata	gaa	gtc	atc	acg	tct	582
Ser	Ile	Ile	Ala	${\tt Asp}$	Arg	Phe	Met	Ser	Ser	Ile	Glu	Val	Ile	Thr	Ser	
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caa	gag	aaa	gaa	atc	acc	ata	aag	aaa	ccc	aat	gga	gag	acc	acc	aag	630
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Thr	Thr	Val	Arg	Ile	Trp	Asn	Glu	Thr	Val	Ser	Asn	Leu		Leu	Met	
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gcc	ctg	aaa	tct	tca	gct	cca	gag	att	ctc	ctt	tca	gta	atc	gag	gtg	726
Ala	Leu	Gly	Ser	Ser	Ala	Pro	Glu	Ile	Leu	Leu	Ser	Val	Ile	Glu	Val	
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Cys	Gly	His	Asn	Phe	Thr	Ala	Gly	Asp	Leu	Gly	Pro	Ser	Thr	Ile	Val	
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ggg	agt	gct	gca	ttc	aac	atg	ttc	atc	atc	att	gcc	ctt	tgt	gtg	tat	822
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_	gtc Val	_	_					_				_	_		870
	gtg Val		_	_		_			_						918
	ttg Leu		_	-				_			_		_	 _	966
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_	agg Arg			_			_		_		_				1062
	aag Lys	_			-										1110
	aag Lys		_		_	_	_				_			-	1158
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	aag Lys	_	_				_	_							1302
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	att Ile														1398

	cat His	_	_	_		-			-	-	_	_			_	1446
	acg Thr 395	_		_	_		_		_	_	_				-	1494
	G1 ^A aaa			_	_	_			_			_	_	_		1542
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	ctg Leu	_	_	_		_				_	_	_				1830
	act Thr															1878
	ttt Phe							-	_	-						1926
gag								~~~								1974

	tat Tyr	_						_	_					-		2022
	gac Asp	_	_					_			_			_		2070
	ata Ile		_	_	_		_	_							_	2118
	ttc Phe								_	_			_	_		2166
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	tac Tyr															2262
	cca Pro									_	_	_		-	_	2310
_	cag Gln		_		_				_			_			_	2358
_	Gly	_			_					_	_					2406
	gaa Glu 715					_	_			_		_		_	_	2454
	aac Asn		_			-		_		_		_		_		2502
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	_	_	_				_		_			_	tgc Cys		2742
	_		_	_					_		_		ctt Leu 840		2790
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		_	-					_				_	tgg Trp		3126

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cataaaaatt atgtataatg aacagaggaa actggcattt gtcatgtcca cccacctgct 3290 gatggaatcc agcttcaaga gcagactctg tactagggcc ggagagagaa ggcatcacct 3350 cccgtttccc aggggcgttc gtcttgttga accaggcatg gaggcagggc catctttacg 3410 tcagctcagc ccagaagcgg tgtgttctcc ccgggttcat aaatccttaa gttctttgat 3470 ttgttttctg tttttgcttg ttttgggtcg gggtagggag gtggttgatg ttagggtttg 3530 gttttggttt tgcaggggga agatcagggt ttgtggtcct cttgtgggag gtgatgtcca 3590 atctcaatgg taaaaatgga aatcaggaag atgactctcc ctttgcccaa aaactttaaa 3650 aattattttg gagtaagaaa ggaaacgggc atggaagaag aaagaagcat gtcttcacca 3710 tattactaaa tttcatgcct tatctctgga gtgggagcag aggtgaagtc ctccctccaa 3770 gaagaaacag gggagctgga atggagccaa gaagagtcat ggttctagat acagtctgat 3830 gtttaaagat acategetge etggeaceet tgttcaacag gtacaaaaac aacatgeeta 3890 gattcccagg aacgcacaaa gtcctttctt atctcttcag cgctggactg tgattagcaa 3950 ggccctgatt ctgatgttct acaccegctg attccccage cctcccatcc caaacccctt 4010 ctccggaccc tttacccctc gtacaaacag gaagaataac tccattcaaa aagcacacca 4070 tcctttccat tcgcatc 4087

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<212> PRT

<213> Bos taurus

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Ser	Tyr 50	Tyr	Cys	Lys	Lys	Gly 55	Val	Ile	Leu	Pro	Ile 60	Trp	Glu	Pro	Gln
Asp	Pro	Ser	Phe	Gly	Asp	Lys	Ile	Ala	Arg	Ala	Thr	Val	Tyr	Phe	Val
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Ala	Met	Val	Tyr	Met	Phe	Leu	Gly	Val	Ser	Ile	Ile	Ala	Asp	Arg	Phe
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Lys	Lys	Pro	Asn	Gly	Glu	Thr	Thr	Lys	Thr	Thr	Val	Arg	Ile	Trp	Asn
•	•	115		-			120	-				125		_	
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Gly	Asp	Leu	Gly	Pro	Ser	Thr	Ile	Val	Gly	Ser	Ala	Ala	Phe	Asn	Met
•	-		-	165					170					175	
Phe	Ile	Ile	Ile	Ala	Leu	Cys	Val	Tyr	Val	Val	Pro	Asp	Gly	Glu	Thr
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Arg	Lys	Ile	Lys	His	Leu	Arg	Val	Phe	Phe	Val	Thr	Ala	Ala	Trp	Ser
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Gly	Val	Val	Glu	Val	Trp	Glu	Gly	Leu	Leu	Thr	Phe	Phe	Phe	Phe	Pro
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Ile	Cys	Val	∀al	Phe	Ala	Trp	Val	Ala	Asp	Arg	Arg	Leu	Leu	Phe	Tyr
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Lys	Tyr	Val	Tyr	Lys	Arg	Tyr	Arg	Ala	Gly	Lys	Gln	Arg	Gly	Met	Ile
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Ile	Glu	His	Glu	Gly	Asp	Arg	Pro	Ser	Ser	Lys	Thr	Glu	Ile	Glu	Met
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Asp	Gly	Lys	Val	Val	Asn	Ser	His	Val	Asp	Ser	Phe	Leu	Asp	Gly	Ala
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Leu	Val	Leu	Glu	Val	Asp	Glu	Arg	Asp	Gln	Asp	Asp	Glu	Glu	Ala	Arg
305					310					315					320
Arg	Glu	Met	Ala	Arg	Ile	Leu	Lys	Glu	Leu	Lys	Gln	Lys	His	Pro	Glu
				325					330					335	
Lys	${\tt Glu}$	Ile	Glu	Gln	Leu	Ile	Glu	Leu	Ala	Asn	Tyr	Gln	Val	Leu	Ser
			340					345					350		
Gln	${\tt Gln}$	${\tt Gln}$	Lys	Ser	Arg	Ala	Phe	Tyr	Arg	Ile	Gln	Ala	Thr	Arg	Leu
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Met	Thr	Gly	Ala	Gly	Asn	Ile	Leu	Lys	Arg	His	Ala	Ala	Asp	Gln	Ala
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Arg	Lys	Ala	Val	Ser	Met	His	Glu	Val	Asn	Thr	Glu	Val	Ala	Glu	Asn
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Asp	Pro	Val	Ser	Lys	Ile	Phe	Phe	Glu	Gln	Gly	Thr	Tyr	Gln	Cys	Leu

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Glu	Asn	Cys	Gly	Thr	Val	Ala	Leu	Thr	Ile	Ile	Arg	Arg	Gly	Gly	Asp
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Pro	Gly	Glu	Thr	Gln	Lys	Glu	Ile	Arg	Val	Gly	Ile	Ile	Asp	Asp	Asp
465					470					475					480
Ile	Phe	Glu	Glu	Asp	Glu	Asn	Phe	Leu	Val	His	Leu	Ser	Asn	Val	Lys
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Val	Ser	Leu	Glu	Ala	Ser	Glu	Asp	Gly	Ile	Leu	Glu	Ala	Ser	His	Val
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His	Val	Ser	Glu	Ser	Ile	Gly	Ile	Met	Glu	Val	Lys	Val	Leu	Arg	Thr
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Glu	Pro	Arg	Leu	Val	Glu	Met	Ser	Glu	Lys	Lys	Ala	Leu	Leu	Leu	Asn
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Glu	Leu	Gly	Gly	Phe	Thr	Ile	Thr	Gly	Lys	Tyr	Leu	Tyr	Gly	${\tt Gln}$	Pro
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Val	Phe	Arg	Lys	Val	His	Ala	Arg	Glu	His	Pro	Leu	Pro	Ser	Thr	Ile
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		675					680					685			
Glu	${\tt Glu}$	Glu	Glu	Arg	Arg	Ile	Ala	Glu	Met	Gly	Arg	Pro	Ile	Leu	Gly
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Glu	His	Thr	Arg	Leu	Glu	Val	Ile	Ile	Glu	Glu	Ser	Tyr	Glu	Phe	Lys
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Ser	Thr	Val	Asp	Lys	Leu	Ile	Lys	Lys	Thr	Asn	Leu	Ala	Leu	Val	Val
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Gly	Thr	Asn	Ser	${\tt Trp}$	Arg	Glu	Gln	Phe	Ile	${\tt Glu}$	Ala	Ile	Thr	Val	Ser
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Ala	${ t Gly}$	Glu	Asp	Asp	Asp	Asp	Asp	Glu	Cys	Gly	Glu	Glu	Lys	Leu	Pro
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785					790					795					800
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				805					810					815	
Asp	Leu	Ala	Ser	His	Phe	Ala	Cys	Thr	Ile	Ala	Leu	Lys	Asp	Ser	Val
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Thr	Ala	Val	Val	Phe	Val	Ala	Leu	${\tt Gly}$	Thr	Ser	Val	Pro	Asp	Thr	Phe
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Gly	Asn	Val	Thr	Gly	Ser	Asn	Ala	Val	Asn	Val	Phe	Leu	Gly	Ile	Gly
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Ser	Cys	Leu	Phe	Val	Leu	Leu	\mathtt{Trp}	Leu	Leu	Tyr	Ile	Phe	Phe	Ser	Ser
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Leu	Glu	Ala	Tyr	Cys	His	Ile	Lys	Gly	Phe						
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